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SEQUENCE ANALYSIS

Get Nucleotide sequences for

EXHIBIT A

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## Clustalw   Your results

Use JalView:		<b>SUBMIT ANOTHER JOB</b>
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### CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: Zlot	470 aa
Sequence 2: 98	351 aa
Sequence 3: 140	257 aa
Sequence 4: 141	257 aa
Sequence 5: 142	291 aa

Start of Pairwise alignments

Aligning....

Sequences (1:2) Aligned. Score:	97
Sequences (1:3) Aligned. Score:	97
Sequences (1:4) Aligned. Score:	97
Sequences (1:5) Aligned. Score:	85
Sequences (2:3) Aligned. Score:	97
Sequences (2:4) Aligned. Score:	97
Sequences (2:5) Aligned. Score:	85
Sequences (3:4) Aligned. Score:	100
Sequences (3:5) Aligned. Score:	96
Sequences (4:5) Aligned. Score:	96

Guide tree      file created: [ebi/extserv/old-work/clustalw-20030820-01221410.dnd]

Start of Multiple Alignment

There are 4 groups

## Aligning...

Group 1: Sequences:	2	Score: 5532
Group 2: Sequences:	2	Score: 7554
Group 3: Sequences:	3	Score: 5539
Group 4: Sequences:	5	Score: 5810

Alignment Score 16213

CLUSTAL-Alignment file created [ebi/extserv/old-work/clustalw-20030820-01221410.aln]

You

**clustalw-20030820-01221410.aln**

CLUSTAL W (1.82) multiple sequence alignment

Zlot  
 98  
 140  
 141  
 142

Zlot	
98	AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 120
140	AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 94
141	AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 94
142	AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 94
	*****

Zlot	
98	LLDGMTCNLRKSFSIHFPLPKKYIEAIQWYGLATPSVFDDLVSNQTLAVSLFSPSH 180
40	LLDGMTCNLRKSFSIHFPLPKKYIEAIQWYGLATPSVFDDLVSNQTLAVSLFSPSH 154
41	LLDGMTCNLRKSFSIHFPLPKKYIEAIQWYGLATPSVFDDLVSNQTLAVSLFSPSH 154
42	LLDGMTCNLRKSFSIHFPLPKKYIEAIQWYGLATPSVFDDLVSNQTLAVSLFSPSH 154
	*****

[illegible]

```
Zlot
98 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRKYVLIPTFWPTPKERNLGLFFLPI 300
140 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRKYVLIPTFWPTPKERNLGLFFLPI 274
141 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRKFISG----- 254
142 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRK----- 250
      KYENIYITRQFVQFDERERHQORPCMLP LNKEERRKNKEL----- 254
      *****;*****

Zlot
98 LIHLCIWVLF AAVDYLLYRLIFSVSKQFQSLPGFEVHLKLHGEKQGTQDI IHDSSFNISV 360
140 LIHLCIWVL -AAVDYLLYRLIFSVSKQFQSLPGFEVHLKLHGEKQGTQDI IHDSSFNISV 333
141 -----FQS----- 257
142 -----KILSMILPLIYLC LNPTV SQNQS FYLRPGFLSV 288

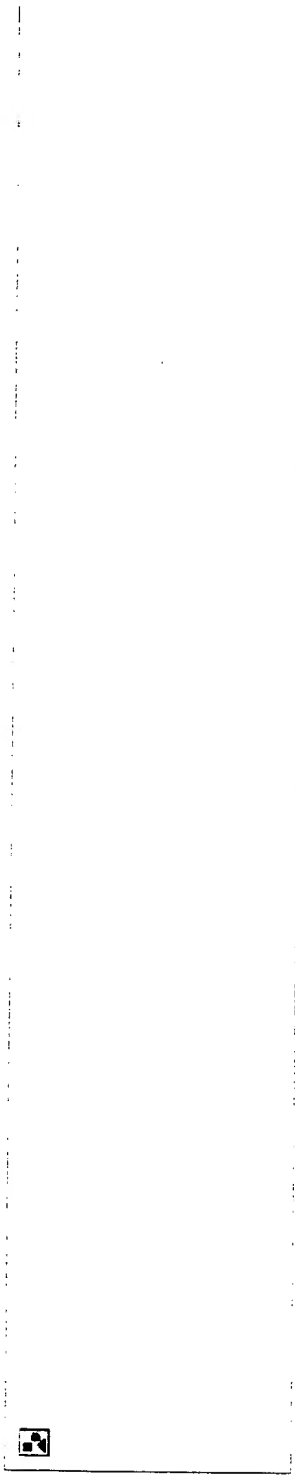
Zlot
98 FEPNCIPKPKFLLSETWVPLSVILLILV MLGLSSILMQLKILVSASFYPSVERKRIQYL 420
140 FEPNCIPK-----WQALKLLAH----- 351
141 -----
142 LFF----- 291

Zlot
98 HAKLLKKRSKQPLGEVKRRLSLYLTKIHF WLPVLK MIRKKQMDMASADKS 470
140 -----
141 -----
142 -----
```

clustalw-20030820-01221410.dnd

```
(
(
(
Zlot:0.01282,
98:0.01282)
:0.03591,
140:-0.02149)
:0.02149,
141:-0.02149,
```

142:0.05262);



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